

2519



SEQUENCE LISTING

<110> Goodwin, Raymond G
Din, Wanwan S.

<120> METHODS OF USE OF THE TACI/TACI-L INTERACTION

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<140> 09/302,863

<141> 1999-04-30

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<170> PatentIn Ver. 2.0

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gtg gct atg aga tcc tgc ccc gaa gag cag tac tgg gat cct ctg ctg 145

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acc tgt gca gcc ttc tgc agg tca ctc agc tgc cgc aag gag caa ggc 241

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Lys Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile

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85

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Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu

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Arg Ser Pro Val Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly

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cac aga ggc tca gaa gca agt cca gct ctc ccg ggg ctg aag ctg agt	481
His Arg Gly Ser Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser	
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gca gat cag gtg gcc ctg gtc tac agc acg ctg ggg ctc tgc ctg tgt	529
Ala Asp Gln Val Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys	
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gcc gtc ctc tgc tgc ttc ctg gtg gcg gtg gcc tgc ttc ctc aag aag	577
Ala Val Leu Cys Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys	
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Arg Gly Asp Pro Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser	
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ccg gcc aag tct tcc cag gat cac gcg atg gaa gcc ggc agc cct gtg	673
Pro Ala Lys Ser Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val	
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agc aca tcc ccc gag cca gtg gag acc tgc agc ttc tgc ttc cct gag	721
Ser Thr Ser Pro Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu	
225 230 235	
tgc agg gcg ccc acg cag gag agc gca gtc acg cct ggg acc ccc gac	769
Cys Arg Ala Pro Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp	
240 245 250	
ccc act tgt gct gga agg tgg ggg tgc cac acc agg acc aca gtc ctg	817
Pro Thr Cys Ala Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu	
255 260 265	
cag cct tgc cca cac atc cca gac agt ggc ctt ggc att gtg tgt gtg	865
Gln Pro Cys Pro His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val	
270 275 280	
cct gcc cag gag ggg ggc cca ggt gca taaatggggg tcagggaggg	912
Pro Ala Gln Glu Gly Gly Pro Gly Ala	
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Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg Thr Cys Ala Ala
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Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp
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His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His
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Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser Pro Val
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130 135 140
Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp Gln Val
145 150 155 160
Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys Ala Val Leu Cys
165 170 175
Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys Arg Gly Asp Pro
180 185 190
Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser Pro Ala Lys Ser
195 200 205
Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val Ser Thr Ser Pro
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Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu Cys Arg Ala Pro
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Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp Pro Thr Cys Ala
245 250 255
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aag aaa aga gaa gaa atg aaa ctg aag gag tgt gtt tcc atc ctc cca      153
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cgg aag gaa agc ccc tct gtc cga tcc tcc aaa gac gga aag ctg ctg      201
Arg Lys Glu Ser Pro Ser Val Arg Ser Ser Lys Asp Gly Lys Leu Leu
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gct gca acc ttg ctg ctg gca ctg ctg tct tgc tgc ctc acg gtg gtg      249
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tct ttc tac cag gtg gcc gcc ctg caa ggg gac ctg gcc agc ctc cgg      297
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gca gag ctg cag ggc cac cac gcg gag aag ctg cca gca gga gca gga      345
Ala Glu Leu Gln Gly His His Ala Glu Lys Leu Pro Ala Gly Ala Gly
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gcc ccc aag gcc ggc ctg gag gaa gct cca gct gtc acc gcg gga ctg      393
Ala Pro Lys Ala Gly Leu Glu Glu Ala Pro Ala Val Thr Ala Gly Leu
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aaa atc ttt gaa cca cca gct cca gga gaa ggc aac tcc agt cag aac      441
Lys Ile Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Asn
             115            120            125

agc aga aat aag cgt gcc gtt cag ggt cca gaa gaa aca gtc act caa      489
Ser Arg Asn Lys Arg Ala Val Gln Gly Pro Glu Glu Thr Val Thr Gln
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gac tgc ttg caa ctg att gca gac agt gaa aca cca act ata caa aaa      537
Asp Cys Leu Gln Leu Ile Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys
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gga tct tac aca ttt gtt cca tgg ctt ctc agc ttt aaa agg gga agt      585
Gly Ser Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser
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gga cat cta att cag agg aag aag gtc cat gtc ttt ggg gat gaa ttg 729
Gly His Leu Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu
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ccc aat aat tcc tgc tat tca gct ggc att gca aaa ctg gaa gaa gga 825
Pro Asn Asn Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly
245 250 255

gat gga gat gtc aca ttt ttt ggt gca ttg aaa ctg ctg tgacctactt 922
Asp Gly Asp Val Thr Phe Phe Gly Ala Leu Lys Leu Leu
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85 90 95

Ala Pro Lys Ala Gly Leu Glu Glu Ala Pro Ala Val Thr Ala Gly Leu
 100 105 110
 Lys Ile Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Asn
 115 120 125
 Ser Arg Asn Lys Arg Ala Val Gln Gly Pro Glu Glu Thr Val Thr Gln
 130 135 140
 Asp Cys Leu Gln Leu Ile Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys
 145 150 155 160
 Gly Ser Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser
 165 170 175
 Ala Leu Glu Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr
 180 185 190
 Phe Phe Ile Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met
 195 200 205
 Gly His Leu Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu
 210 215 220
 Ser Leu Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu
 225 230 235 240
 Pro Asn Asn Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly
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 35 40 45
 Tyr His Ile Glu Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu
 50 55 60
 Arg Thr Arg Ser Gly Asn Ser Ser Gln Asn Ser Arg Asn Lys Arg Ala
 65 70 75 80
 Val Gln Gly Pro Glu Thr Val Thr Gln Asp Cys Leu Gln Leu Ile
 85 90 95

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Pro	Trp	Leu	Leu	Ser	Phe	Lys	Arg	Gly	Ser	Ala	Leu	Glu	Glu	Lys	Glu
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			145												
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			165												
Arg	Ile	Cys	Ile	Gln	Asn	Met	Pro	Glu	Thr	Leu	Pro	Asn	Asn	Ser	Cys
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			225												
			230												